SEQUENCE LISTING

<110> Barta, Andrea
Lopato, Sergyi
Kalyna, Maria
Dorner, Silke

<120> Splicing Factor

<130> SONN:013US

<140> UNKNOWN
<141> 2001-10-23

<150> PCT/AT00/00100
<151> 2000-04-20

<150> A 727/99
<151> 1999-04-23

<160> 22

<170> PatentIn Ver. 2.1

<210> 1
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 1
aaatgagctc aaatgtatat gtatggaaaa acc 33

<210> 2
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 2
aatgagctcg aaacgatatc ttcaaaaaaa aac 33

<210> 3
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 3

aaactggatc cagaacaatc taacgctttc tcg 33

<210> 4
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 4
atataggatc ctcaaccaga uaucacaggt g 31

<210> 5
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 5
aaatatctag agatctcaaa tcgacgacc 29

<210> 6
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 6
atataggatc ccattttacc tcgatggac 29

<210> 7
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 7
aatgagctct gtgtcacctg ctagatcc 28

<210> 8
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 8

atataggatc cagatatcac aggtgaaac 29

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 9
ataggatcca ggagcagaag tcccaaggca aag 33

<210> 10
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 10
aaagtcgaca gaaggtagag gagatcttga tc 32

<210> 11
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 11
aaactaagct tggtatcttc ttccctgcaa g 31

<210> 12
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 12
aaacctaggc ggctactcag ctgatacctc agagcag 37

<210> 13
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 13

aaactaagct taaatattga accggcctcg gttc 34

<210> 14
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 14
aaactggatc ctcttcctgt tggtcgtcga cgatttg 37

<210> 15
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 15
aaactggatc ctcttccttt atcaaatcc 29

<210> 16
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 16
atataccatg ggtagccgat ggaatcgtac 30

<210> 17
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:Primer

<400> 17
atataccatg ggcagtcgtt cgag 24

<210> 18
<211> 4044
<212> DNA
<213> Unknown

<220>
<223> Description of the unknown organism:genome
atSRp30

<400> 18
agacaaagat gcttacttct taaacatgtt cgaggtttat tgaaaatgat caccagcttc 60
taactatggt atcttcttcc ctgcaagcga acagtggaag atgattgata acggaaatat 120
cggaacatca ctcaacaaac caaaaatttg gacatcatat cgcaacaaat tcaataggaa 180
aaatactgaa attccaaaac agaaaaacca aacggaacag agcaggaact cacggactga 240
gagagaccgt ggacggtgtc acggcggaaa atggtcttgg acggagttac taatcggcga 300
attgagattt gagaggtggt agtagaggaa ccgagagaat gtttctctca aaaaaatccc 360
caagtgtttc cgatctagtg tctcttttgt ccaaaaacga cagtgtttag gaaacctagg 420
agaatgaatg acccgatggt ccgaatccga ttcgaaattg gttcgaattg taataactaa 480
catacaatat tccggtttga atgataagaa aaaacacatt cgatccggtt agaacaatat 540
attaacaggc ccattaaaac atatgggccg atcttgatca actgggctat tcatcgttga 600
tacatgcggc cgcacaggat taaaatccag ttccgtttta taaaaggata ctagtttcca 660
aacgaacggt ggttgtctcc tttccagaac aatctaacgc tttctcgaac atcttcttct 720
tcttctttct cgaaattatt tttccagtaa tcaatttctt ctcttctaga tttttacagg 780
aactaatttt ctgctctgag gtatcagatg agtagccgat ggaatcgtac gatctacgtt 840
gggaatttgc ctggagatat tcgcaagtgt gaggttgaag atctcttcta caaggtttga 900
aaatttcctc ttttctctcg ataaaaattg aattcattat gactagtttg ggttcataaa 960
tttgcaattc tgtcttgctg agacaattta aatcgactct tatgtatatt tgtttcagta 1020
tggaccaatt gtggacattg atttgaagat tccaccgaga cctcctggtt atgcctttgt 1080
cgaggtatat tgatcaagta caaatttgtt tttttcttct tcttgtaata gtataggcta 1140
atgactaaga tagtttgtta ttggtggcag tttgaagatc ctcgtgatgc agacgatgca 1200
atttatggac gtgatggtta tgattttgat gggtgtcgac ttcgggttag taaacgcatg 1260
atgaaagcta gcttaatttt ctgtaatttc ttgtaaaggt gttatctttg tgtgatgttt 1320
ttaggttgag attgcacatg gtggtcgtag attttcacca tcagttgata ggtacagcag 1380
cagctacagt gcgagccgtg caccttcaag acgctctgac taccgcggtt tgtagagtct 1440
tctcgattgt gttatttggt gttgtgtaaa attttatatt tgaaaactca tttttactac 1500
ctaaacatgt agtgcttgtg accggattac cgccttctgc ttcgtggcag gaccttaagg 1560
taagggacac tatatagtct ttttctctga atgttggttc tctatatcat gttttggatt 1620
tatctctttt ctgaaatgat gttatttgct atttacgggt gattaggatc acatgcgcaa 1680
agctggagat gtctgcttct ctgaagtttt ccctgaccgt aaaggtgagt tgacattcga 1740
tagtttggat aagcttttttg attgatgtgt tagtaaatta gtctttgtga aggagaatag 1800
gtgttaagca tctgaactgc taaactcaca ttcagtattt ctttgtaggc atgtctgggg 1860
ttgtggatta tagcaactat gatgatatga agtacgcagt aagttttata tctttgcaac 1920
gcaaatgttc ctggacttat gccttagact gcttttgttt catagtatac cgagctgaat 1980
ttatcttcct ggaggccagt gttggatctt tgatgttccc ttaaaatttt tgatgtgaca 2040
gataaggaaa cttgatgcca ctgaatttcg aaatgctttc tctagtgctt atatacgggt 2100
atgttgtatt gctttctttg attttgttaa gcataagtgg atatggagtc atctctgaat 2160
ttactgttca ggtgagggaa tatgagtcga ggagtgtgag tcgaagccca gatgattcta 2220
aaagctatag aagcaggagt cggagccgtg gtccaagctg tagctatagt agcaagagca 2280
ggaggtcttt tttttttttt ttttttcata aacctaagac atataaggga tttttattgt 2340
aacttattta tgaaattaac tgacttctaa atgcaatgca gtgtgtcacc tgctagatcc 2400
atttccccgc gttcacggcc ccttagtcgt tctcgctcgc tatacagctc tgtctcaagg 2460
tatgagtgtt agatttgtat cattattata tatgtagtta ccccttcatg gatcacttgt 2520
tcttgcatag tgaactcctt actagcttta ttacttacaa ctaagcacct tttgttgctt 2580
ccgtacacag ttgaatttgt ttgagtcttt tttccctcat agtggactag tctattgtca 2640
cttgattttc ttcctttgtt gatgttttct atgtcatgca aactccaata tgggtaaagg 2700
ttacctcctt gtttgggatt accagagttc cttttcattt cttacacgtg aatgtgtttg 2760
ttttttatgt tttgagttct tgacagagat gctcccatca tatttagtcc ttttcctttc 2820
tctttgtgtc gttctcttct ggatgtttcc ttctgataaa gctttacttc ttaacttttt 2880
tccagcgacg gtgaatttat tacgtatcaa cctcaatatc cgacctataa tttaaagaac 2940
acttagctag atgttcactt ttgaaaattt atttctatcg gaagggggca gatgatttct 3000
gaggcatgtc ctcgatcatt taccgtgatt acaattgtat tgcgttgttt gtttctagat 3060
ctggctcact gctacgagct ggggattgga tctagatggg tcatctagat ggattcttgg 3120
actggattta caaagctgga ttagcatgaa ctgaacttct gttttacggt ctggtctggt 3180
ctggtactcc gcgcgtatca gctgtaggat ctgatcgcaa agttttggac tatgattact 3240

ctgattcctc aatatattta tctttttgac aatagtggat tctgtgttga gttcttttct 3300
aggacagcat ttaagctccc gggactagat gggagatggt cagtaaattt ctttgttatg 3360
ccacacttac atggggtttt tcggtcttgc tgcaggtccc aatcaagatc aaaatcaaga 3420
tcaagatcaa gatcgaattc tccagtttca cctgtggtaa gtctaaaagc tgaaccttct 3480
ttaattcaca atccatgtgt ttgtttaaat acctgctcac tttggttgtt cttcaatcaa 3540
caccaactta acgaaatcat gagacagact ataaaatttg aagagtctgt agaacgacta 3600
ggtctcacca acctctgtgt gcactaaaaa tcgcctctcc aagtgtttca gcaacataat 3660
ctacctctgt catgtgttat catttcttct tctcttaacg gtattacata ttatgttttg 3720
caggtgatat ctggttgaaa atgaaaactg gccactggct gtacccgaat cgtctcaagc 3780
ttctcaggct ccactgctaa tagaatttga ttccgatttg ggattattat actggtcttc 3840
ttgtatggga cgaccaatat gtctttctag ttttagttgt gaacctggaa ttggtctgtt 3900
attgtgtcat taaaaagccg gaaactctgt ctcggctgca taataaagtt catcagacat 3960
tgtgttgggt gtggtgaggt ttttccatac atatacattt acattacaac tactggtgtc 4020
ttttatgatt atcttaaact aaac 4044

<210> 19
<211> 279
<212> PRT
<213> Unknown

<220>
<223> Description of the unknown organism:genome
atSRp30

<400> 19

Met	Ser	Ser	Arg	Trp	Asn	Arg	Thr	Ile	Tyr	Val	Gly	Asn	Leu	Pro	Gly
1				5				10					15		
Asp	Ile	Arg	Lys	Cys	Glu	Val	Glu	Asp	Leu	Phe	Tyr	Lys	Tyr	Gly	Pro
		20					25					30			
Ile	Val	Asp	Ile	Asp	Leu	Lys	Ile	Pro	Pro	Arg	Pro	Pro	Gly	Tyr	Ala
	35					40					45				
Phe	Val	Glu	Phe	Glu	Asp	Pro	Arg	Asp	Ala	Asp	Asp	Ala	Ile	Tyr	Gly
50					55					60					
Arg	Asp	Gly	Tyr	Asp	Phe	Asp	Gly	Cys	Arg	Leu	Arg	Val	Glu	Ile	Ala
65				70					75					80	
His	Gly	Gly	Arg	Arg	Phe	Ser	Pro	Ser	Val	Asp	Arg	Tyr	Ser	Ser	Ser
			85					90					95		
Tyr	Ser	Ala	Ser	Arg	Ala	Pro	Ser	Arg	Arg	Ser	Asp	Tyr	Arg	Val	Leu
		100					105					110			
Val	Thr	Gly	Leu	Pro	Pro	Ser	Ala	Ser	Trp	Gln	Asp	Leu	Lys	Asp	His
	115					120					125				
Met	Arg	Lys	Ala	Gly	Asp	Val	Cys	Phe	Ser	Glu	Val	Phe	Pro	Asp	Arg
130					135					140					
Lys	Gly	Met	Ser	Gly	Val	Val	Asp	Tyr	Ser	Asn	Tyr	Asp	Asp	Met	Lys
145				150					155					160	

Tyr Ala Ile Arg Lys Leu Asp Ala Thr Glu Phe Arg Asn Ala Phe Ser
165 170 175

Ser Ala Tyr Ile Arg Val Arg Glu Tyr Glu Ser Arg Ser Val Ser Arg
180 185 190

Ser Pro Asp Asp Ser Lys Ser Tyr Arg Ser Arg Ser Arg Ser Arg Gly
195 200 205

Pro Ser Cys Ser Tyr Ser Ser Lys Ser Arg Ser Val Ser Pro Ala Arg
210 215 220

Ser Ile Ser Pro Arg Ser Arg Pro Leu Ser Arg Ser Arg Ser Leu Tyr
225 230 235 240

Ser Ser Val Ser Arg Ser Gly Ser Leu Leu Arg Ala Gly Asp Trp Ile
245 250 255

Ser Gln Ser Arg Ser Lys Ser Arg Ser Arg Ser Arg Ser Asn Ser Pro
260 265 270

Val Ser Pro Val Ile Ser Gly
275

<210> 20
<211> 1132
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:atSRp34/SR1

<400> 20
aggagcagaa gtcccaaggc aaagtcttca cgtaggtccc ctgcaaaatc tacatcaaga 60
tctcctggcc cccgctcgaa gtcaaggtca ccgtctccaa gaaggtaatg atttgattcc 120
ttttcagaat gcaccaggca acattactta gtcggtagat tttcctgtga agtttatgaa 180
aatctgatta gaaaagtcat tgttgatgct caaagttctt gttgattgag catatactgg 240
ttttttgttg acacctgctg tttgctcgtc attattgtcc cttcttactc catccttata 300
tttagatgct tagccctttt ctggttaaga tttgcgagat tggccttaca tttttagcat 360
ttttaaatat gctctttttct ttcctgagaa gaaaatggtt ttgtttcata gatatggatt 420
tacatacgac tagaaaatgg aaattaatat ctggatggaa attgattgtt gacaagtgtt 480
tcgtctaaga ggtatgggaa actttggaat agagactttg cttttcgtgg cttcctgata 540
tagtattcac taatttacat tgctgctaga tggataacag tggagacatt ggatcacttg 600
gatcacaata ttatatcggg atttctgtaa aactatattg gctcgatgga ttgacaatat 660
ggaatctggg ctctcttggg acgtacgtgg ctcatttggc aacacaagtt tttttcgcca 720
catggcttat aaaacctctg tcctatcacc tatgttttaa ctaagtagca gaatagtttg 780
gtttatgttc ctttttttta tttgttgcaa cttcttaatc tctgtgagat agaaggagag 840
gctccaggac cttgctgaac agtataaaac acaacatgtt tggatttttg aatctgagtt 900
tcttttcttg gacttttgca gatcgcgttc aagatcaaga tctcctctac cttctgtgag 960
taacaagatc caacttgtga cccctctttt attttgacat aatcttctgt tttacattgt 1020
tcgttatctt aatagctttt ctgtatcaca ggttcagaag gaaggaagca agagccctag 1080
caagccaagt ccagccaaga gtcctatcca cactaggagt ccatcgaggt aa 1132

<210> 21
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:atSRp34/SR1

<400> 21
Arg Ser Arg Ser Pro Lys Ala Lys Ser Ser Arg Arg Ser Pro Ala Lys
1 5 10 15

Ser Thr Ser Arg Ser Pro Gly Pro Arg Ser Lys Ser Arg Ser Pro Ser
20 25 30

Pro Arg Arg Tyr Gly Phe Thr Tyr Asp Ser Arg Ser Arg Ser Arg Ser
35 40 45

Pro Leu Pro Ser Val Gln Lys Glu Gly Ser Lys Ser Pro Ser Lys Pro
50 55 60

Ser Pro Ala Lys Ser Pro Ile His Thr Arg Ser Pro Ser Arg
65 70 75

<210> 22
<211> 248
<212> PRT
<213> Homo sapiens

<400> 22
Met Ser Gly Gly Gly Val Ile Arg Gly Pro Ala Gly Asn Asn Asp Cys
1 5 10 15

Arg Ile Tyr Val Gly Asn Leu Pro Pro Asp Ile Arg Thr Lys Asp Ile
20 25 30

Glu Asp Val Phe Tyr Lys Tyr Gly Ala Ile Arg Asp Ile Asp Leu Lys
35 40 45

Asn Arg Arg Gly Gly Pro Pro Phe Ala Phe Val Glu Phe Glu Asp Pro
50 55 60

Arg Asp Ala Glu Asp Ala Val Tyr Gly Arg Asp Gly Tyr Asp Tyr Asp
65 70 75 80

Gly Tyr Arg Leu Arg Val Glu Phe Pro Arg Ser Gly Arg Gly Thr Gly
85 90 95

Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Arg Gly Arg Tyr
100 105 110

Gly Pro Pro Ser Arg Arg Ser Glu Asn Arg Val Val Val Ser Gly Leu
115 120 125

```
Pro Pro Ser Gly Ser Trp Gln Asp Leu Lys Asp His Met Arg Glu Ala
    130                 135                 140

Gly Asp Val Cys Tyr Ala Asp Val Tyr Arg Asp Gly Thr Gly Val Val
145                 150                 155                 160

Glu Phe Val Arg Lys Glu Asp Met Thr Tyr Ala Val Arg Lys Leu Asp
                165                 170                 175

Asn Thr Lys Phe Arg Ser His Glu Gly Glu Thr Ala Tyr Ile Arg Val
            180                 185                 190

Lys Val Asp Gly Pro Arg Ser Pro Ser Tyr Gly Arg Ser Arg Ser Arg
        195                 200                 205

Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Asn Ser Arg Ser Arg
    210                 215                 220

Ser Tyr Ser Pro Arg Arg Ser Arg Gly Ser Pro Arg Tyr Ser Pro Arg
225                 230                 235                 240

His Ser Arg Ser Arg Ser Arg Thr
                245
```